

Protein Micro-Crystallography with a SPring-8 Micro-Beam Beamline

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Structure determination with protein crystallography is often prevented by the small size of the crystals. However proteins involved in important target of current crystallography, such as membrane proteins or protein complexes, tend to show difficulties in growing their crystal size. Therefore, demands for achieving protein micro-crystallography are getting larger and larger. At SPring-8, we are developing RIKEN Targeted Proteins beamline (BL32XU)¹⁾ focused on micron-order crystals.

In order to realize the protein micro-crystallography, development of beamline optics and data collection system to provide high signal-to-noise ratio (S/N) data from weak diffractions should be essential. We have designed the beamline with the focused beam size of 1 μ m. A small sized and highly brilliant X-ray beam with the size of 1 μ m will provide high S/N data by both increasing reflection intensities and reducing background scattering around sample.

A hybrid in-vacuum undulator developed at SPring-8 will be equipped for highly brilliant light source. X-rays from the undulator is monochromatized by liquid-N₂ cooled double crystal monochromator, and will be focused by using K-B mirrors fabricated with Elastic Emission Machinery²⁾. The ray trace simulation based on our optical design shows the minimum beam size at sample position corresponds to 1 x 1 μ m² with 6 x 10¹⁰ photons/sec/ μ m². The beam size can be changed up to the maximum size of 20 x 20 μ m² according to the size of sample crystal.

In addition, developments of indispensable components to achieve protein micro-crystallography with micro-beam, such as high-precision diffractometer, laser tweezers system for micro-crystal handling, advanced software system to suppress radiation damage and so on, are progressing. Utilization of the micro-beam not only for micro-crystals but for 'low-quality' ones will also be targeted. One of them is probing a single-crystal component from a heterogeneous protein crystal using the micro-beam. We will present the current status and the future prospects of protein micro-crystallography at SPring-8.

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1) http://beamline.harima.riken.jp/en/bl_info/bl32xu_info.html

2) <http://www.upst.eng.osaka-u.ac.jp/21coe/english/index.html>

3) http://www.tanpaku.org/e_index.html